GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-9
Perfect score: 20
Sequence: 1 tgaggtgcgggtggaagtgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	3	AAZ31439	Aaz31439 Human neu
	2	20	100.0	20	9	ADA74691	Ada74691 GTI3609 a
c	3	15.8	79.0	23	10	ABZ26016	Abz26016 Orthosomy
	4	15.2	76.0	60	6	ABN49870	Abn49870 Human spl
	5	15.2	76.0	100	8	ACD79788	Acd79788 E. coli K
c	6	15	75.0	24	2	AAV55815	Aav55815 Multimeri
c	7	15	75.0	24	2	AAV55817	Aav55817 Multimeri
c	8	14.8	74.0	25	9	ACI45513	Aci45513 Human mic
	9	14.8	74.0	48	2	AAQ28729	Aaq28729 Sequence
c	10	14.8	74.0	48	2	AAQ28730	Aaq28730 Sequence
	11	14.4	72.0	25	9	ACI86896	Aci86896 Human mic
c	12	14.4	72.0	25	9	ACH59512	Ach59512 DNA targe
	13	14.4	72.0	60	6	ABN48299	Abn48299 Human spl
c	14	14.2	71.0	20	12	ADJ23951	Adj23951 Human end
c	15	14.2	71.0	20	12	ADJ23488	Adj23488 Human end
c	16	14.2	71.0	21	2	AAQ70342	Aaq70342 Antisense
c	17	14.2	71.0	24	10	ABZ58545	Abz58545 PCR prime
c	18	14.2	71.0	30	2	AAQ31897	Aaq31897 PCR prime
c	19	14.2	71.0	30	3	AAA95218	Aaa95218 G+C rich
c	20	14.2	71.0	30	10	ADC66453	Adc66453 Human Fra
	21	14.2	71.0	50	2	AAX52367	Aax52367 Probe use
	22	14.2	71.0	50	3	ADC78471	Adc78471 Human PRO
	23	14.2	71.0	50	4	AAF72525	Aaf72525 Human PRO
c	24	14.2	71.0	50	4	AAL33769	Aal33769 Human SNP
c	25	14.2	71.0	50	4	AAL33771	Aal33771 Human SNP
c	26	14.2	71.0	50	4	AAL33772	Aal33772 Human SNP
	27	14.2	71.0	50	8	ACA60124	Aca60124 Human sec
	28	14.2	71.0	50	8	ACD07524	Acd07524 Novel hum
	29	14.2	71.0	50	8	ABX71572	Abx71572 Human sec
	30	14.2	71.0	50	8	ACH06904	Ach06904 Human sec
	31	14.2	71.0	50	8	ABX96141	Abx96141 Human sec
	32	14.2	71.0	50	8	ACA05462	Aca05462 Human sec
	33	14.2	71.0	50	8	ACD20129	Acd20129 Human sec
	34	14.2	71.0	50	8	ACA54932	Aca54932 Novel sec
	35	14.2	71.0	50	9	ACD19767	Acd19767 Human sec
	36	14.2	71.0	50	9	ADB29356	Adb29356 Human sec
	37	14.2	71.0	50	9	ADA18212	Ada18212 Human sec
	38	14.2	71.0	50	9	ACD66914	Acd66914 Human sec
	39	14.2	71.0	50	9	ACD83075	Acd83075 Human PRO
	40	14.2	71.0	50	9	ADA16187	Ada16187 Human sec
	41	14.2	71.0	50	9	ADA42332	Ada42332 Human sec
	42	14.2	71.0	50	9	ACD23253	Acd23253 Human PRO
	43	14.2	71.0	50	9	ADA16611	Ada16611 Human sec
	44	14.2	71.0	50	9	ADA13040	Ada13040 Human sec
	45	14.2	71.0	50	9	ADA41908	Ada41908 Human sec

ALIGNMENTS

RESULT 1
AAZ31439
ID AAZ31439 standard; DNA; 20 BP.
XX
AC AAZ31439;
XX
DT 07-FEB-2000 (first entry)
XX
DE Human neuropilin mRNA specific antisense oligo GTI3609.
XX
KW Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;
KW papilloma; diabetic retinopathy; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9955855-A2.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-CA000324.
XX
PR 23-APR-1998; 98US-0082791P.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Lee YS;
XX
DR WPI; 2000-023357/02.
XX
PT Antisense oligonucleotides that inhibit neuropilin expression, useful for
PT treating cancer.
XX
PS Claim 4; Page 16; 57pp; English.
XX
CC Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit
CC human neuropilin expression. The antisense oligonucleotides can be used
CC to inhibit the growth or metastasis of a mammalian tumor and inhibit
CC neovascularisation. The oligonucleotides may be used to treat various
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas,
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of
CC the mouth, throat, larynx and lung, genitourinary cancers such as

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CC   cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC   cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC   cancer, head and neck cancers, and nervous system cancers, as well as
CC   benign lesions such as papillomas. The methods may be used to treat
CC   neovascularisation disorders such as diabetic retinopathy, and
CC   retinopathy of prematurity and age related macular degeneration
XX
SQ   Sequence 20 BP; 3 A; 2 C; 11 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGAGGTGCGGGTGGAAGTGC 20
              ||||||||||||||||||||
Db          1 TGAGGTGCGGGTGGAAGTGC 20


RESULT 2
ADA74691
ID   ADA74691 standard; DNA; 20 BP.
XX
AC   ADA74691;
XX
DT   20-NOV-2003  (first entry)
XX
DE   GTI3609 antisense oligonucleotide targeted to human neuropilin mRNA.
XX
KW   neuropilin; VEGF165R; vascular endothelial growth factor receptor;
KW   cytostatic; growth; tumour metastasis; angiogenesis; gene therapy;
KW   GTI3609; antisense; human; ss.
XX
OS   Homo sapiens.
XX
PN   US2003083274-A1.
XX
PD   01-MAY-2003.
XX
PF   22-APR-1999;   99US-00296264.
XX
PR   23-APR-1998;   98US-0082791P.
XX
PA   (WRIG/) WRIGHT J A.
PA   (YOUN/) YOUNG A H.
PA   (LEEY/) LEE Y S.
XX
PI   Wright JA,  Young AH,  Lee YS;
XX
DR   WPI; 2003-576622/54.
XX
PT   New antisense oligonucleotide that inhibits neuropilin expression, useful
PT   for inhibiting growth of mammalian tumor or inhibiting metastasis of a
PT   mammalian tumor.
XX
PS   Claim 1; Page 5; 27pp; English.
XX
CC   The invention relates to a novel antisense oligonucleotide that inhibits
CC   the expression of neuropilin, also known as VEGF165R (vascular
CC   endothelial growth factor receptor). The oligonucleotide of the invention
CC   demonstrates cytostatic activity and may be useful for inhibiting the
CC   growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
CC   mammals. Furthermore, the oligonucleotide may be utilised during gene
CC   therapy. The current sequence is that of the GTI3609 antisense
CC   oligonucleotide of the invention which is targeted to human neuropilin
CC   mRNA.
XX
SQ   Sequence 20 BP; 3 A; 2 C; 11 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGAGGTGCGGGTGGAAGTGC 20
              ||||||||||||||||||||
Db          1 TGAGGTGCGGGTGGAAGTGC 20


RESULT 3
ABZ26016/c
ID   ABZ26016 standard; DNA; 23 BP.
XX
AC   ABZ26016;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Orthosomycin biosynthetic gene related oligonucleotide UEVB-S1.
XX
KW   Orthosomycin; biosynthesis; everninomicin; avilamycin; PCR; primer;
KW   probe; ss.
XX
OS   Synthetic.
XX
PN   WO200279505-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-CA000432.
XX
PR   28-MAR-2001; 2001US-0279095P.
PR   30-MAR-2001; 2001US-0279709P.
PR   20-APR-2001; 2001US-0285214P.
XX
PA   (ECOP-) ECOPIA BIOSCIENCES INC.
XX
PI   Farnet CM,  Zazopoulos E,  Staffa A;
XX
DR   WPI; 2003-058435/05.
XX
PT   Identifying orthosomycin biosynthetic gene, gene fragment or gene
PT   cluster, by detecting presence of nucleic acid sequence corresponding to
PT   17 of flambamycins protein families.
XX
PS   Example 6; Page 109; 511pp; English.
XX
CC   The invention relates to identifying orthosomycin biosynthetic genes and
CC   its fragment/gene cluster (ABZ66670-ABZ666813), comprising detecting the
CC   presence of a nucleic acid sequence coding for a polypeptide (ABP99207-
CC   ABP99362). The method is useful for identifying an orthosomycin
CC   biosynthetic gene, gene fragment or gene cluster, especially an
CC   everninomicin-type or avilamycin-type orthosomycin biosynthetic gene,
CC   gene fragment or gene cluster. The method is useful for detecting the
CC   presence of any organism that contains DNA for the production of
CC   orthosomycins (both everninomicin-type orthosomycins and avilamycin-type
CC   orthosomycins) regardless of the level at which genes for orthosomycin
CC   production are expressed by the organism or the amount of orthosomycin
CC   produced by the organism. This allows for the detection of new
CC   orthosomycin natural products, not produced by the organism. The present
CC   sequence is that of an oligonucleotide designed to be used as a PCR
CC   primer or probe for identifying orthosomycin biosynthetic loci in other
CC   organisms
XX
SQ   Sequence 23 BP; 4 A; 11 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             79.0%;  Score 15.8;  DB 10;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GAGGTGCGGGTGGAAGTGC 20
              || |||||||||| |||||
Db         21 GAAGTGCGGGTGGTAGTGC 3


RESULT 4
ABN49870
ID   ABN49870 standard; DNA; 60 BP.
XX
```

```
AC   ABN49870;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human spliced transcript detection oligonucleotide SEQ ID NO:22618.
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss.
XX
OS   Homo sapiens.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB001903.
XX
PR   28-JUL-2000; 2000US-0221607P.
PR   02-MAY-2001; 2001US-0287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of a
PT   genome, useful for detecting tissue-, pathology-, and developmental-
PT   specific genes.
XX
PS   Example 1; SEQ ID NO 22618; 47pp; English.
XX
CC   The present invention describes oligonucleotide libraries for detecting
CC   messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC   )transcriptome comprises messenger RNAs transcribed from multiple
CC   transcription units that populate a genome. The library comprises several
CC   oligonucleotides, each capable of hybridising selectively to a set of
CC   messenger RNAs transcribed from a given transcription unit of the genome,
CC   which encodes one or more messenger RNA splice variants. The
CC   oligonucleotide libraries are useful for detecting mRNAs from a
CC   biological sample, in expression profiling studies, in qualitatively or
CC   quantitatively characterising the corresponding transcriptome, and in
CC   detecting RNA transcripts and splice variants of human or animal
CC   transcriptomes. The libraries may also be used as specialised mini
CC   libraries to detect transcripts of a sub-transcriptome under a particular
CC   biological or pathological state, and so allowing the detection of tissue
CC   - and pathology-specific genes such as those genes only expressed in
CC   specific tissue under a specific pathological condition; to detect
CC   developmental specific genes; and to detect RNA transcripts and splice
CC   variants of a transcriptome of a patient suffering from a particular
CC   disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC   rats, humans and mice, which are used in the exemplification of the
CC   present invention. N.B. The sequence data for this patent did not form
CC   part of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 60 BP; 17 A; 12 C; 18 G; 13 T; 0 U; 0 Other;

  Query Match             76.0%;  Score 15.2;  DB 6;  Length 60;
  Best Local Similarity   85.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGAGGTGCGGGTGGAAGTGC 20
              |||||||| |||||| || |
Db         25 TGAGGTGCTGGTGGATGTCC 44


RESULT 5
ACD79788
ID   ACD79788 standard; DNA; 100 BP.
XX
AC   ACD79788;
XX
DT   19-SEP-2003  (first entry)
XX
DE   E. coli K12 MG1655 biochip probe SEQ ID 11064.
XX
KW   Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX
OS   Escherichia coli.
XX
PN   EP1260592-A1.
XX
PD   27-NOV-2002.
XX
PF   17-MAY-2001; 2001EP-00112179.
XX
PR   17-MAY-2001; 2001EP-00112179.
XX
PA   (MWGB-) MWG-BIOTECH AG.
XX
PI   Donner H,  Drescher B,  Huber A,  Weber J;
XX
DR   WPI; 2003-241155/24.
XX
PT   Biochip containing probes complementary with open reading frames in
PT   Escherichia coli K12, useful for detecting gene expression and expression
PT   patterns.
XX
PS   Claim 3; Page 1724; 2004pp; German.
XX
CC   This invention describes a novel biochip comprising probe spots, each
CC   containing many identical probes. The probes are nucleotide sequences of
CC   30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC   least one includes a segment of at least 20 bases identical with, or
CC   complementary to, a segment of an open reading frame (orf) of Escherichia
CC   coli K12. The biochip is used for specific detection of gene expression
CC   in K12 and for determining the gene expression pattern, e.g. for
CC   diagnostic determination of which E. coli strains are present in the gut,
CC   and to determine the effects of e.g. growth media on gene expression. The
CC   biochip provides as comprehensive as possible detection of the K12
CC   genome, with simultaneous analysis of many different genes with a single
CC   device, and comparison of gene expression between K12 and its mutants or
CC   other E. coli strains in a single experiment. Apart from qualitative and
CC   quantitative information about gene expression, it also allows
CC   measurements of population densities for the various strains. The use of
CC   synthetic oligonucleotides for preparation of probes allows free
CC   variation in probe length and ensures high purity (and thus selectivity,
CC   reactivity and reproducibility); also synthetic probes are generally
CC   shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC   ACD81540 represent oligonucleotide probes used with the biochip described
CC   in the invention
XX
SQ   Sequence 100 BP; 28 A; 16 C; 30 G; 26 T; 0 U; 0 Other;

  Query Match             76.0%;  Score 15.2;  DB 8;  Length 100;
  Best Local Similarity   85.0%;  Pred. No. 3.8e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGAGGTGCGGGTGGAAGTGC 20
              |||||||| | |||| |||
Db         31 TGAGGTGCGCGAGGAAATGC 50


RESULT 6
AAV55815/c
ID   AAV55815 standard; DNA; 24 BP.
XX
AC   AAV55815;
XX
DT   27-AUG-2003  (revised)
DT   18-NOV-1998  (first entry)
XX
DE   Multimerisation of minimal motifs using primer ZGS2.
XX
```

KW Fusion protein; stabilising polypeptide; proteolytic degradation;
KW resistance; half-life; autoimmune disease; inflammation; nitro drug;
KW IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
KW nitroreductase protein; enzyme therapy; prodrug therapy; protease;
KW cancer; pathological condition; minimal motif; PCR primer; ss.
XX
OS Synthetic.
OS Human herpesvirus 4.
XX
PN WO9822577-A1.
XX
PD 28-MAY-1998.
XX
PF 17-NOV-1997; 97WO-IB001508.
XX
PR 15-NOV-1996; 96US-0030986P.
PR 25-JUN-1997; 97US-0048945P.
XX
PA (MASU/) MASUCCI M G.
XX
PI Masucci MG;
XX
DR WPI; 1998-312463/27.
XX
PT New fusion proteins resistant to proteolytic degradation - comprising a
PT core protein with a stabilising polypeptide comprising a peptide sequence
PT containing glycine repeats.
XX
PS Disclosure; Page 72; 120pp; English.
XX
CC Sequences shown in AAV55812 to AAV55827 represent primers used in the
CC course of the invention for the multimerisation of minimal motifs. The
CC invention provides a method for increasing the resistance of a core
CC protein to proteolytic degradation that comprises linking or inserting
CC onto or into the core protein a stabilising polypeptide of formula
CC [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly
CC residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr
CC and n can be anything between 1-66. X, Y and Z need not be identical from
CC n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising
CC polypeptide can be linked onto or inserted into a nucleic acid encoding a
CC core protein. The fusion proteins of the invention are more resistant to
CC degradation by proteases and, thus, have a longer half-life than the
CC unfused core protein. The products can be used for treating autoimmune
CC diseases, cancer and inflammation. In particular, the core protein may be
CC an IkappaB regulator protein for the treatment of inflammatory bowel
CC disease, or a nitroreductase protein which can activate nitro drugs in
CC enzyme/prodrug therapy to treat cancer or other pathological conditions.
CC The fusion proteins can also be used in diagnostic methods such as in
CC vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 24 BP; 4 A; 14 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGGAA 16
||||||||||||||||
Db 15 GAGGTGCGGGTGGAA 1

RESULT 7
AAV55817/c
ID AAV55817 standard; DNA; 24 BP.
XX
AC AAV55817;
XX
DT 27-AUG-2003 (revised)
DT 18-NOV-1998 (first entry)
XX
DE Multimerisation of minimal motifs using primer ZGR2.
XX
KW Fusion protein; stabilising polypeptide; proteolytic degradation;
KW resistance; half-life; autoimmune disease; inflammation; nitro drug;
KW IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
KW nitroreductase protein; enzyme therapy; prodrug therapy; protease;
KW cancer; pathological condition; minimal motif; PCR primer; ss.
XX
OS Synthetic.
OS Human herpesvirus 4.
XX
PN WO9822577-A1.
XX
PD 28-MAY-1998.
XX
PF 17-NOV-1997; 97WO-IB001508.
XX
PR 15-NOV-1996; 96US-0030986P.
PR 25-JUN-1997; 97US-0048945P.
XX
PA (MASU/) MASUCCI M G.
XX
PI Masucci MG;
XX
DR WPI; 1998-312463/27.
XX
PT New fusion proteins resistant to proteolytic degradation - comprising a
PT core protein with a stabilising polypeptide comprising a peptide sequence
PT containing glycine repeats.
XX
PS Disclosure; Page 72; 120pp; English.
XX
CC Sequences shown in AAV55812 to AAV55827 represent primers used in the
CC course of the invention for the multimerisation of minimal motifs. The
CC invention provides a method for increasing the resistance of a core
CC protein to proteolytic degradation that comprises linking or inserting
CC onto or into the core protein a stabilising polypeptide of formula
CC [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly
CC residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr
CC and n can be anything between 1-66. X, Y and Z need not be identical from
CC n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising
CC polypeptide can be linked onto or inserted into a nucleic acid encoding a
CC core protein. The fusion proteins of the invention are more resistant to
CC degradation by proteases and, thus, have a longer half-life than the
CC unfused core protein. The products can be used for treating autoimmune
CC diseases, cancer and inflammation. In particular, the core protein may be
CC an IkappaB regulator protein for the treatment of inflammatory bowel
CC disease, or a nitroreductase protein which can activate nitro drugs in
CC enzyme/prodrug therapy to treat cancer or other pathological conditions.
CC The fusion proteins can also be used in diagnostic methods such as in
CC vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 24 BP; 3 A; 14 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGGAA 16
||||||||||||||||
Db 15 GAGGTGCGGGTGGAA 1

RESULT 8
ACI45513/c
ID ACI45513 standard; DNA; 25 BP.
XX
AC ACI45513;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 45504.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 45504; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 7 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGAGGTGCGGGTGGAAGT 18
||||||| ||| |||||||
Db 24 TGAGGTTCGGCTGGAAGT 7

RESULT 9
AAQ28729
ID AAQ28729 standard; DNA; 48 BP.
XX
AC AAQ28729;
XX
DT 25-MAR-2003 (revised)
DT 27-FEB-1993 (first entry)
XX
DE Sequence of oligonucleotide 2119 corresponding to the linking peptide
DE between VH and VL domains of plasmid pFvCD3-H-gamma-3.
XX
KW Chimaeric polypeptide; cell surface CD4 molecule; HIV type 1; HIV-1;
KW human immunodeficiency virus; antigen binding site; cytotoxic T-; cell;
KW CD3 molecule; T-cell receptor complex; PCR; ss.

XX
OS Synthetic.
XX
PN EP505908-A1.
XX
PD 30-SEP-1992.
XX
PF 18-MAR-1992; 92EP-00104656.
XX
PR 27-MAR-1991; 91EP-00810220.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Karjalainen K, Lanzavecchia A, Traunecker A;
XX
DR WPI; 1992-325228/40.
XX
PT DNA encoding chimeric bi:specific polypeptide(s) e.g. CD4 and CD3 binding
PT site - for treating HIV infection, and also cancers e.g. ovarian
PT carcinoma(s) or leukaemia(s).
XX
PS Example; Page 10; 19pp; English.
XX
CC Plasmid pFvCD3-H-gamma-3 comprises a DNA sequence coding for the variable
CC regions of the heavy and the light chain (VH and VL) of an anti-human CD3
CC antibody (FvCD3) derived from hybridoma TR66 and for all domains except
CC the first of the constant regions of the heavy chain of the human
CC immunoglobulin G3. The second strand synthesis of the sequences coding
CC for the VL and VH-domains of the anti-CD3 hybridoma TR66 was performed by
CC T4 DNA polymerase and 5' oligonucleotides 1570 for VH and 1569 for VL
CC sequences. Final amplification was then achieved by using the above
CC mentioned oligonucleotides and 3' oligonucleotides 1354 and 1239j
CC complementary to mouse gamma-HC (immunoglobulin - gamma - heavy chain)
CC and C-kappa (constant domain of immunoglobulin kappa-light chain) genes.
CC The L region (initiation codon and leader sequence for eukaryotic
CC secretion) of the Sp6 HC gene contg. the small intron was amplified by
CC using 5' olionucleotides 1609 and 3' oligonucleotides 1610 which are also
CC complementary (20 bp) to oligonucleotides 1570 at its 5' end (ie at the
CC beginning of the amplified VH fragment. Junctional and flanking
CC olibonucleotides were designed and used to link the L region from Sp6 VH
CC and VL fragments together in one 35 PCR reaction: the flanking 5' and 3'
CC oligonucleotides were 1609 and 2768 respectively, the latter having
CC complementarity to the end for the mouse J-kappa-5 sequence. The
CC oligonucleotide 2139 which links VH to VL fragments had 20 bp
CC complementarities to the end of the JH2-sequence and to oligonucleotide
CC 1569, ie to the 5' end of the VL sequence. Finally, a synthetic piece of
CC DNA with SalI compatible ends (oligonucleotides 2119 and 2120)
CC corresponding to the linking peptide between VH and VL domains, was
CC cloned into a SalI site of the intermediate plasmid to give plasmid
CC pFvCD3-H-gamma-3. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 48 BP; 10 A; 3 C; 24 G; 11 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 2; Length 48;
Best Local Similarity 88.9%; Pred. No. 5.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGGAAGTG 19
||||| | ||||||||||
Db 16 GAGGTTCTGGTGGAAGTG 33

RESULT 10
AAQ28730/c
ID AAQ28730 standard; DNA; 48 BP.
XX
AC AAQ28730;
XX
DT 25-MAR-2003 (revised)
DT 27-FEB-1993 (first entry)
XX
DE Sequence of oligonucleotide 2120 corresponding to the linking peptide
DE between VH and VL domains of plasmid pFvCD3-H-gamma-3.

XX
KW Chimaeric polypeptide; cell surface CD4 molecule; HIV type 1; HIV-1;
KW human immunodeficiency virus; antigen binding site; cytotoxic T-; cell;
KW CD3 molecule; T-cell receptor complex; PCR; ss.
XX
OS Synthetic.
XX
PN EP505908-A1.
XX
PD 30-SEP-1992.
XX
PF 18-MAR-1992; 92EP-00104656.
XX
PR 27-MAR-1991; 91EP-00810220.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Karjalainen K, Lanzavecchia A, Traunecker A;
XX
DR WPI; 1992-325228/40.
XX
PT DNA encoding chimeric bi:specific polypeptide(s) e.g. CD4 and CD3 binding
PT site - for treating HIV infection, and also cancers e.g. ovarian
PT carcinoma(s) or leukaemia(s).
XX
PS Example; Page 10; 19pp; English.
XX
CC Plasmid pFvCD3-H-gamma-3 comprises a DNA sequence coding for the variable
CC regions of the heavy and the light chain (VH and VL) of an anti-human CD3
CC antibody (FvCD3) derived from hybridoma TR66 and for all domains except
CC the first of the constant regions of the heavy chain of the human
CC immunoglobulin G3. The second strand synthesis of the sequences coding
CC for the VL and VH-domains of the anti-CD3 hybridoma TR66 was performed by
CC T4 DNA polymerase and 5' oligonucleotides 1570 for VH and 1569 for VL
CC sequences. Final amplification was then achieved by using the above
CC mentioned oligonucleotides and 3' oligonucleotides 1354 and 1239j
CC complementary to mouse gamma-HC (immunoglobulin - gamma - heavy chain)
CC and C-kappa (constant domain of immunoglobulin kappa-light chain) genes.
CC The L region (initiation codon and leader sequence for eukaryotic
CC secretion) of the Sp6 HC gene contg. the small intron was amplified by
CC using 5' olionucleotides 1609 and 3' oligonucleotides 1610 which are also
CC complementary (20 bp) to oligonucleotides 1570 at its 5' end (ie at the
CC beginning of the amplified VH fragment. Junctional and flanking
CC olibonucleotides were designed and used to link the L region from Sp6 VH
CC and VL fragments together in one 35 PCR reaction: the flanking 5' and 3'
CC oligonucleotides were 1609 and 2768 respectively, the latter having
CC complementarity to the end for the mouse J-kappa-5 sequence. The
CC oligonucleotide 2139 which links VH to VL fragments had 20 bp
CC complementarities to the end of the JH2-sequence and to oligonucleotide
CC 1569, ie to the 5' end of the VL sequence. Finally, a synthetic piece of
CC DNA with SalI compatible ends (oligonucleotides 2119 and 2120)
CC corresponding to the linking peptide between VH and VL domains, was
CC cloned into a SalI site of the intermediate plasmid to give plasmid
CC pFvCD3-H-gamma-3. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 48 BP; 11 A; 24 C; 3 G; 10 T; 0 U; 0 Other;

```
  Query Match             74.0%;  Score 14.8;  DB 2;  Length 48;
  Best Local Similarity   88.9%;  Pred. No. 5.5e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GAGGTGCGGGTGGAAGTG 19
              ||||| | ||||||||||
Db         37 GAGGTTCTGGTGGAAGTG 20
```

RESULT 11
ACI86896
ID ACI86896 standard; DNA; 25 BP.
XX
AC ACI86896;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 86887.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 86887; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 6 A; 5 C; 9 G; 5 T; 0 U; 0 Other;

```
  Query Match             72.0%;  Score 14.4;  DB 9;  Length 25;
  Best Local Similarity   93.8%;  Pred. No. 8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GTGCGGGTGGAAGTGC 20
              |||| ||||||||||
Db          4 GTGCCGGTGGAAGTGC 19
```

RESULT 12
ACH59512/c
ID ACH59512 standard; DNA; 25 BP.
XX
AC ACH59512;
XX
DT 17-OCT-2003 (first entry)
XX
DE DNA target sequence #8648 useful in array for genetic analyses.

```
XX
KW   Gene expression analysis; array; hybridisation; genetic variation;
KW   tag-labelled compound; gene family; in situ hybridisation;
KW   library screening; Southern hybridisation; northern hybridisation;
KW   dot-blot hybridisation; gene sequence; mutation detection;
KW   target sequence; probe; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   US2003082596-A1.
XX
PD   01-MAY-2003.
XX
PF   08-AUG-2002; 2002US-00215112.
XX
PR   08-AUG-2001; 2001US-0311040P.
XX
PA   (MITT/) MITTMANN M.
XX
PI   Mittmann M;
XX
DR   WPI; 2003-576608/54.
XX
PT   New probe array useful e.g. for monitoring gene expression levels, for
PT   analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT   comprises multiple nucleic acid probes.
XX
PS   Claim 1; SEQ ID NO 8648; 9pp; English.
XX
CC   The present invention relates to nucleic acid sequences that are
CC   complementary to particular genes, and can be used as probes for a
CC   variety of analyses such as gene expression analysis. Each probe
CC   comprises 9 or more consecutive nucleotides from at least one of 14936
CC   nucleotide sequences defined in the patent, or their perfect sense match,
CC   sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC   The probes may be used in an array comprising at least 10 distinct
CC   nucleic acid probes. The array is useful in monitoring gene expression
CC   levels by hybridisation to a DNA library, in analysing genetic
CC   variations, and in hybridising tag-labelled compounds. The probes are
CC   useful for identifying family members of a gene. The probes are also
CC   useful in in situ hybridisations, in screening cDNA or genomic libraries
CC   (or derived subclones) for additional clones containing segments of DNA
CC   that have been previously isolated and sequenced, in Southern, northern,
CC   or dot-blot hybridisation of genomic DNA to identify or detect the
CC   sequence of any gene or detect specific mutations in any gene, and in
CC   mapping the 5' termini of mRNA molecules by primer extensions. The
CC   nucleic acid sequences of the invention are also useful as PCR primers.
CC   The invention provides a large collection of nucleic acid sequences
CC   complementary to particular genes with a wide range of analytical uses.
CC   ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC   The sequence data for this patent was obtained in electronic format
CC   directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 25 BP; 4 A; 10 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 14.4;  DB 9;  Length 25;
  Best Local Similarity   93.8%;  Pred. No. 8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GAGGTGCGGGTGGAAG 17
              ||||||| ||||||||
Db         24 GAGGTGCCGGTGGAAG 9


RESULT 13
ABN48299
ID   ABN48299 standard; DNA; 60 BP.
XX
AC   ABN48299;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human spliced transcript detection oligonucleotide SEQ ID NO:21047.
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss.
XX
OS   Homo sapiens.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB001903.
XX
PR   28-JUL-2000; 2000US-0221607P.
PR   02-MAY-2001; 2001US-0287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of a
PT   genome, useful for detecting tissue-, pathology-, and developmental-
PT   specific genes.
XX
PS   Example 1; SEQ ID NO 21047; 47pp; English.
XX
CC   The present invention describes oligonucleotide libraries for detecting
CC   messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC   )transcriptome comprises messenger RNAs transcribed from multiple
CC   transcription units that populate a genome. The library comprises several
CC   oligonucleotides, each capable of hybridising selectively to a set of
CC   messenger RNAs transcribed from a given transcription unit of the genome,
CC   which encodes one or more messenger RNA splice variants. The
CC   oligonucleotide libraries are useful for detecting mRNAs from a
CC   biological sample, in expression profiling studies, in qualitatively or
CC   quantitatively characterising the corresponding transcriptome, and in
CC   detecting RNA transcripts and splice variants of human or animal
CC   transcriptomes. The libraries may also be used as specialised mini
CC   libraries to detect transcripts of a sub-transcriptome under a particular
CC   biological or pathological state, and so allowing the detection of tissue
CC   - and pathology-specific genes such as those genes only expressed in
CC   specific tissue under a specific pathological condition; to detect
CC   developmental specific genes; and to detect RNA transcripts and splice
CC   variants of a transcriptome of a patient suffering from a particular
CC   disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC   rats, humans and mice, which are used in the exemplification of the
CC   present invention. N.B. The sequence data for this patent did not form
CC   part of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 60 BP; 16 A; 9 C; 24 G; 11 T; 0 U; 0 Other;

  Query Match             72.0%;  Score 14.4;  DB 6;  Length 60;
  Best Local Similarity   93.8%;  Pred. No. 8.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 AGGTGCGGGTGGAAGT 18
              |||||||||| |||||
Db          6 AGGTGCGGGTTGAAGT 21


RESULT 14
ADJ23951/c
ID   ADJ23951 standard; DNA; 20 BP.
XX
AC   ADJ23951;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human endothelial lipase antisense oligonucleotide, SEQ ID 2349.
XX
```

```
KW   Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW   Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW   cardiovascular disorder; metabolic syndrome X; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 4 nucleotides in length. Also all
FT                   cytidine residues are 5-methylcytidines"
XX
PN   WO2004009541-A2.
XX
PD   29-JAN-2004.
XX
PF   18-JUL-2003; 2003WO-US022410.
XX
PR   19-JUL-2002; 2002US-0397106P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Bhat BG;
XX
DR   WPI; 2004-132912/13.
XX
PT   New antisense oligonucleotide for modulating endothelial lipase
PT   expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT   high density lipoprotein or cardiovascular disorders.
XX
PS   Claim 3; SEQ ID NO 2349; 1007pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADJ21603-
CC   ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC   (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC   with and inhibits the expression of EL. The antisense oligonucleotides
CC   are useful for modulating the expression of endothelial lipase in cells
CC   or tissues to treat diseases associated with EL expression, such as
CC   dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC   disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC   used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ   Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             71.0%;  Score 14.2;  DB 12;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 9.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGAGGTGCGGGTGGAAGTG 19
              |||| | |||| |||||||
Db         19 TGAGATTCGGGAGGAAGTG 1


RESULT 15
ADJ23488/c
ID   ADJ23488 standard; DNA; 20 BP.
XX
AC   ADJ23488;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human endothelial lipase antisense oligonucleotide, SEQ ID 1886.
XX
KW   Antilipaemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW   Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW   cardiovascular disorder; metabolic syndrome X; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 4 nucleotides in length. Also all
FT                   cytidine residues are 5-methylcytidines"
XX
PN   WO2004009541-A2.
XX
PD   29-JAN-2004.
XX
PF   18-JUL-2003; 2003WO-US022410.
XX
PR   19-JUL-2002; 2002US-0397106P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Bhat BG;
XX
DR   WPI; 2004-132912/13.
XX
PT   New antisense oligonucleotide for modulating endothelial lipase
PT   expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
PT   high density lipoprotein or cardiovascular disorders.
XX
PS   Claim 3; SEQ ID NO 1886; 1007pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADJ21603-
CC   ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
CC   (ADJ25517), where the antisense oligonucleotide specifically hybridises
CC   with and inhibits the expression of EL. The antisense oligonucleotides
CC   are useful for modulating the expression of endothelial lipase in cells
CC   or tissues to treat diseases associated with EL expression, such as
CC   dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
CC   disorder or metabolic syndrome X. In addition, the oligonucleotides are
CC   used for diagnostics, prophylaxis, or as research reagents or kits.
XX
SQ   Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             71.0%;  Score 14.2;  DB 12;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 9.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TGAGGTGCGGGTGGAAGTG 19
              |||| | |||| |||||||
Db         20 TGAGATTCGGGAGGAAGTG 2


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Job time : 173.4 secs
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